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(54) **Method and apparatus for cell counting and cell classification.**

(57)   A method and an apparatus for analyzing a
material within a container, such as blood with-
in a capillary in a volumetric cytometry system
provides for detecting the edges of the con-
tainer, counting the cells within the container,
characterizing the cells within the container.
and evaluating channels of data which contain
information relevant to more than one of the
detectable characteristics of the cells. A scan-
ner scans a container of material including
certain cells. Sampling circuitry is coupled to
the scanner to generate scanned images of the
material in the container. Two or more scanned
images are generated based on fluorescence
data from dyes that have overlapping spectra.
The two scanned images are processed using a
linear regression analysis among correspond-
ing pixels in the scanned images near certain
cells to characterize relative contents of two
fluorescing dyes in a target cell. Target cells are
identified from the scanned images using pro-
cessing resources which identify a peak sample
within a neighborhood, and compare the ampli-
tude of the peak with the amplitude of pixels on
the perimeter of the neighborhood. Upon iden-
tifying a target cell in this manner, data from the
plurality of scanned images corresponding to
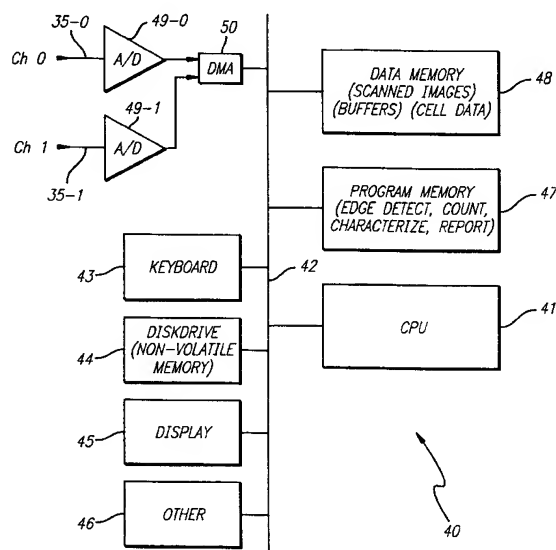the identified cell are saved for further analysis.

FIG. 2

EP 0 681 177 A1

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CONTINUING APPLICATION DATA

The present application is a continuation-in-part of Serial Number 08/018,762 filed February 17. 1993 entitled "Method and Apparatus for Volumetric Capillary Cytometry", assigned to the same assignee of the present application.

CROSS-REFERENCE TO RELATED APPLICATION

The present application is related to U.S. patent application entitled "Method and Apparatus for Volumetric Capillary Cytometry" invented by Baer et al, filed on 2nd May 1994 under Serial No. 08/236,342 and owned by the same Assignee. The related application is incorporated by reference as if fully set forth herein.

BACKGROUND OF THE INVENTION

Field of the Invention

The present invention relates generally to the processing of volumetric capillary cytometry data for the purpose of counting and characterizing cells or cell constituents in a volume of material.

Description of Related Art

The optical analysis of biological specimens, such as blood, has widespread applications. There are many computer controlled instruments in the market for providing such analysis, including flow cytometers, automated blood cell analyzers and blood cell classifiers.

As described in the above cross-referenced application, a volumetric cytometry instrument has many advantages. In particular, the amount of blood being analyzed is controllable, the handling of the blood is reduced, and analyzed samples of blood can be stored for further processing.

However, the processing of blood samples in a volumetric system raises a number of problems. Particularly if counting of blood cells is required, it is necessary to analyze the entire volume in the capillary or other container which holds the material to be analyzed. Blood cells on the side of a container may be difficult to detect, if the analysis instrument is not calibrated for the precise dimensions of the container. For instance, in Kamentsky, U.S. Patent No. 5,072,382, samples of blood were applied to a slide. A region to be analyzed was defined by synchronization pulses in the scanning apparatus. (See column 14, lines 49-63 of Kamentsky). Synchronization pulses in the scanning mechanism cannot be precisely aligned with a container such as a capillary or cuvette for a blood sample because of the variations in the shapes of such containers, and variations in the alignment of mounts for the containers in the scanning mechanism. It will be appreciated that the ability to precisely mount and manufacture containers is quite advanced. However, the scanning of containers for the purposes of processing cells may require resolution on the micron scale.

An additional difficulty arises because of the characteristics of dyes used to mark target cells. For instance, when analyzing cells for the presence of specific antibodies, it is common to tag the cells with dyes which fluoresce with a particular spectrum in response to an excitation beam. If more than one antibody is to be detected, more than one dye is used. However, the fluorescence spectrums of various dyes may overlap. Thus, it is difficult to fully process the information in detected fluorescence generated by plural dyes with overlapping spectra.

Furthermore, when it is necessary to count a particular number of target cells within a volume, to achieve a statistically valid count, a relatively large sample must be used. A large sample of blood, when it is scanned on the micron scale, can generate very large amounts of data. It is important for practical analysis machines that the data be processed in a reasonable amount of time. For instance, as described in the above cross-referenced application, the sample can scan for the presence of two dyes with overlapping spectra, with two,channels of data. Each channel of data includes information relevant to both dyes. Further, the scan involves about 10,000 lines of 200 pixels each resulting in 2 million samples per channel, which for 2 bytes per

sample in 2 channels amounts to a total of 8 megabytes of raw data.

Furthermore, the fluorescence monitoring techniques are susceptible to a low signal-to-noise ratio. Thus, it is important to be able to process these large amounts of data with high background noise to accurately characterize and identify target cells within the volume, particularly when unbound antibody is present.

Accordingly, it is desirable to provide a method and apparatus for processing data from a volumetric cytometry system which is robust and accurate. Further, the system should be relatively fast and operate in a system having a relatively low memory requirement.

SUMMARY OF THE INVENTION

Embodiments of the present invention provide a method and an apparatus for analyzing a sample of cells or cell constituents, including but not limited to blood, within a capillary in a volumetric cytometry system. According to a preferred embodiment, the sample cells or cell constituents have one or more detectable characteristics. The system provides for detecting the edges of the container, counting the cells or cell constituents within the container, characterizing the cells or cell constituents within the container, and evaluating channels of data which contain information relevant to more than one of the detectable characteristics of the cells or cell constituents.

Accordingly, a currently preferred embodiment comprises a scanner for scanning a container of sample including target cells or cell constituents. Data sampling circuitry is coupled to the scanner to generate scanned images of the sample in the container. According to one aspect, the scanner and data sampling circuitry produce a plurality of channels of data, and a corresponding plurality of scanned images. A processing system is coupled to the sampling circuitry, and includes resources to count and/or characterize the target cells or cell constituents in response to the scanned images.

These processing resources, according to one aspect, are capable of processing the scanned image, which includes information relevant to more than one of the detectable characteristics of the cells or cell constituents, to distinguish such detectable characteristics. Such resources may include software for performing a correlation analysis between the scanned image having information relevant to more than one characteristic and another scanned image in the plurality of scanned images. In one preferred system, two scanned images are generated based on fluorescence data from dyes that have overlapping spectra. The two scanned images are processed using a linear regression analysis among corresponding pixels in the scanned images near target cells to characterize relative contents of two fluorescing dyes in a target cell or cell constituents.

In another preferred embodiment, target cells or cell constituents are identified from the scanned images using processing resources which identify a peak pixel within a neighborhood, and compare the amplitude of the peak with the amplitude of pixels on the perimeter of the neighborhood. If the peak pixel value exceeds the perimeter pixel values by more than a predetermined threshold, then the resources characterize the neighborhood as containing a target cell. Upon identifying a target cell in this manner, segments of data from the plurality of scanned images corresponding to the identified cell can be saved for further analysis, such as the linear regression analysis discussed above.

Further, according to another preferred embodiment, in addition to determining a relative contribution from more than one dye in a scanned image, a parameter indicating the intensity of the fluorescence of a target cell or cell constituents is determined by filtering the identified segments of data from the plurality of scanned images based upon the expected characteristics of target cells or cell constituents. For example, in one arrangement, the segments are filtered by defining a neighborhood of pixels for each identified segment in the scanned images, wherein the neighborhood is larger than the expected size of the target cell. The pixels within the neighborhood are processed to compensate for background noise and generate an intensity value for the target cell within the neighborhood, based solely on pixel values within the neighborhood. For instance, this processing may involve a matched filter multiplying the intensity values of the neighborhood of a cell by a set of values which reflects the expected intensity profile of a typical cell. The resulting products are summed to yield an amplitude estimate which optimizes signal to noise ratio for that cell. The perimeter of the neighborhood is determined based on the expected shape of the target cells or cell constituents within the neighborhood.

According to yet another preferred embodiment, the processing resources perform edge detection, and ignore contributions to the scanned images which fall outside of the detected edges of the container.

In the preferred system, the cells or cell constituents are characterized using a slope value determined from the linear regression analysis over a neighborhood defined for a target cell between two scanned images of the cell generated from overlapping fluorescence spectra of two dyes. Using the linear regression analysis, a "slope value" is determined for each target cell. This slope value is then multiplied by the intensity value of the neighborhood in one of the scanned images to produce an analysis coordinate. The cell or cell constituents

is characterized based upon the position of the analysis coordinate on a characterization graph. The characterization graph is defined with a first region within which target cells or cell constituents having one dye should fall, a second region within which target cells or cell constituents having the second dye should fall, and a third region within which target cells or cell constituents stained with both dyes should fall. The regions are defined based on the background signal characteristics of the scanned images for the purposes of signal immunity and more accurate characterizations.

There is also provided a method for analyzing the sample within such a container. In one embodiment the method includes the following:

scanning the material with a detector to generate a plurality of channels of data, in which at least one of the channels may contain information relevant to more than one of a plurality of detectable characteristics of the target cells or cell constituents;

sampling the plurality of channels of data to produce a plurality of scanned images of the sample; and

analyzing the plurality of scanned images to characterize the target cells or cell constituents in response to the plurality of channels of data, including processing the scanned image corresponding to the one channel which includes information relevant to more than one characteristic to distinguish such detectable characteristics, processing at least one of the plurality of scanned images to identify segments in the plurality of scanned images containing target cells or cell constituents, filtering identified segments of data based upon expected characteristics of target cells or cell constituents to generate respective intensity values for the identified segments, and characterizing the target cells or cell constituents based on the intensity value in at least one of the plurality of scanned images for a particular segment, and a value based on correlation analysis (such as the slope in a linear regression analysis) between two scanned images of a segment of data.

The system may also include analyzing at least one of the scanned images to detect the edges of the container and ignoring data found outside of the detected edges. Furthermore, the process of characterizing the intensity value for a particular segment of data may include defining a neighborhood of pixels for each identified segment, the neighborhood being larger than the expected size of the target cell and processing the pixels within the neighborhood to compensate for background signal and generate an intensity value for the target cell or cell constituents within the neighborhood.

Other aspects and advantages of the present invention can be seen upon review of the figures, the detailed description, and the claims which follow.

BRIEF DESCRIPTION OF THE FIGURES

Fig. 1 is a schematic block diagram of a scanner apparatus with a data processing system embodying the present invention.

Fig. 2 is a schematic block diagram of the data processing system used in combination with the system of Fig 1.

Fig. 3 is a schematic diagram illustrating the scanning process used in the scanner of Fig. 1.

Fig. 4 schematically illustrates an organization of data in the scanned images generated by sampling the output of the scanner of Fig. 1.

Fig. 5 is a plot of a representative scanned image from the system according to Fig. 1.

Figs. 6A and 6B together make up a flow chart for the basic data processing loop for the system embodying the present invention.

Fig. 7 illustrates the overlapping spectra of two dyes which are analyzed embodying the present invention.

Fig. 8 is a graph illustrating the linear regression analysis used in the characterization of cells embodying the present invention.

Fig. 9 illustrates a cell classification graph used for classifying cells based on channels of data which include overlapping information, embodying the present invention.

Fig. 10 is a flow chart illustrating the generation of background noise indices embodying the present invention.

Fig. 11 is a flow chart illustrating the edge detection process embodying the present invention.

Fig. 12 is a flow chart of the process used for detecting cells embodying the present invention.

Fig. 13 is a flow chart illustrating the process for linear regression analysis embodying the present invention.

DETAILED DESCRIPTION

A detailed description of preferred embodiments of the present invention is provided with respect to the figures. Figs. 1 and 2 illustrate a typical hardware environment. Figs. 3-13 provide an explanation of the proc-

essing resources used to count and characterize target cells or cell constituent.

As can be seen in Fig. 1, an apparatus for volumetric capillary cytometry is provided. The machine is designed to process material within a capillary 10, which has a known volume. In the preferred system, the capillary may be rectangular in cross-section, having a width of about 0.4 millimeters to 1.5 millimeters, a length of about 40 millimeters, and a depth of about 25 to 225 microns, and in one embodiment, 100 microns. This capillary is suitable for detecting or characterizing a variety of cells or cell constituents. In one embodiment, it is used for the characterization of a CD3/CD4 assay in which concentration of CD3 and CD4 antibodies are to be determined. In this type of assay, there are typically three populations present: CD3 positive cells stained with a Cy5 labelled antibody only; CD4 cells stained with both a CyS labelled CD3 antibody and a CyFr labelled CD4 antibody. Monocytes are stained with the CyFr labelled CD4 antibody only. It is found that the cells of interest in this assay are about 10 microns in diameter and are well classified using a capillary of the dimensions outlined above. It will be appreciated that the present invention is not limited to the characterization of a CD3/CD4 assay.

According to one method, a biological fluid, such as whole uncoagulated blood, can be reacted with an excess amount of a binding agent that contains a fluorophone excitable at a given wavelength. The fluorescently-labeled binding agent is selected to react with binding sites present within the sample. For example, a fluorescently-labeled antibody directed to the CD4 cell surface marker present on some leukocyte blood subclasses is reacted with a sample of whole blood. The labeled binding agents and the binding sites, i.e. labeled anti-CD4 antibodies and the surfaces of CD4-bearing leukocytes in the example form fluorescent complexes that will emit a signal when used with the apparatus embodying the present invention.

After the fluidic sample is reacted with the labeled binding agent, it is diluted and the into capillary 10. Minimal processing of components of the biological fluid nor separation of bound and unbound binding agent is required at any point in the practice of the method embodying the present invention. An optical scan is made of the sample in a volumetric manner and fluorescence emission is sequentially recorded from each illuminated columnar region.

Fluorescence emission occurs from both the binding agent-binding site complexes and from the free binding agent but a more intense signal relative to background level comes from areas where the binding agent is clustered, i.e. cells or cell constituents exhibiting binding sites to which the binding agent is directed. Therefore, a signal of heightened fluorescence corresponds to a cell or cell constituents, and is recorded as such. When the fluorophores with which the anti-CD4 antibodies are labeled and excited in the given example, the fluorescence emitted and recorded as an event signifies the presence of a leukocyte that expresses the CD4 antigen.

The enumeration may occur in an absolute volume, depending on a desired application, by noting the beginning and ending points of the lengthwise scan of the capillary tube and measuring incremental steps therebetween. This quantitation of all of the fluorescent targets in a fixed, precise volume is a powerful method of quickly obtaining detailed population data.

Fluorophores that activate at different wavelengths can be combined with binding agents directed to different binding sites, so that the presence of multiple reaction moieties in the sample can be detected. From the precise known volume of the capillary tube that has been scanned, a quick reading will identify the number of cells or cell constituents of a particular subclass per unit volume that are present in the sample. To illustrate, this method can quickly distinguish and enumerate the monocyte granulocyte or lymphocyte subsets of a given volume of a blood sample through reaction of the whole sample with differentially-excitable fluorescently-labeled antibodies directed to the cell surface antigens. The T-cell leukocytes can be directed to CD3, CD4, and CD8. The optical system is simply set to excite each fluorophore at its crucial wavelength and a detection channel is created to correspond to the emission wavelength of each fluorophore. Alternatively, a ratio can be obtained without counting a precise volume e.g. this is a rapid technique for obtaining CD4/CD8 T-cell ratios, important in determining the progression of AIDS.

When an assay is performed to determine leukocyte subclasses in whole uncoagulated blood using the technique, a two or three minute wait between placement of the reacted sample into the capillary tube and the optical scan allows for the natural density of the numerous red blood cells present in the sample to cause settling of the red blood cells to the bottom of the capillary tube and the subsequent displacement of the white blood cells. This natural buoyant effect causes a resultant location of the white blood cells near the upper portion of the capillary tube and assists in fluorescence detection because of the top-down scan geometry of the present invention. Because of this effect, coincidence of targets is also negligible.

The scanner is based on use of a laser 11, such as a helium - neon laser (as shown), an ion laser, a semiconductor laser or the like which generates a laser beam along path 12. Laser 11 preferably emits in the 600 to 1000 nm range. The laser beam along path 12 passes through a beam splitter 13, such that a portion of the beam is diverted to a power meter 14 for monitoring the laser output power. The main beam passes through

the beam splitter 13 to a narrow line filter 15, which selects the wavelength of interest generated by the laser 11. Next, a dichroic beam splitter 16 receives the beam which passes through the filter 15. The dichroic beam splitter diverts the selected output from the laser toward a steering mirror 17. The steering mirror 17 diverts the beam to a folding mirror or prism 18. From the folding mirror or prism 18, the beam is directed to a scanner 19.

The scanner 19 allows transverse and longitudinal scanning of the laser beam across the sample capillary 10. The scanner assembly includes a galvanometer mounted mirror 25 which rotates a few degrees back and forth in a rapid fashion at about 20 - 200 Hz (peak-to-peak 6 - 12°). The beam is deflected by the galvanometer mounted mirror 25 to a first lens 22, through a second lens 23 and through an objective lens 24 to the capillary 10. Two lenses 22 and 23 are designed to be confocal, that is, they are separated along the optical path by their focal length, and they have equal focal lengths. It is not necessary that the lenses be confocal, but they must have overlapping focal planes. Similarly, the distance between lens 23 and the objective lens 25 of the microscope must be precisely controlled so that the beam, as it is rotated by the galvanometer mounted mirror 25, appears to be rotating about a virtual point directly in front of the microscope objective.

As schematically illustrated by ghosted outline 39, the scanning assembly 19 is designed to move longitudinally along the capillary 10 for a distance of about 40 millimeters.

A variety of other scanner mechanisms can be used as suits a particular application of the invention.

The whole scanner assembly 19 is controlled by computer 30, as schematically illustrated by line 26.

The beam impinging upon the outer wall of capillary 10 traverses the wall and illuminates a columnar region of the sample causing fluorescent emission from the sample. Light collection occurs in an epi-illumination manner. The emitted fluorescence is collected by microscope objective 24 and directed back, as a retrobeam. Microscope objective 24 has a central portion for passage of incident beam and uniform depth of focus of the incident beam through capillary 10. Because flourescent emission is over a very wide angle, flourescent collection occurs over a wider portion of microscope objective 24

Fluorescence given off by the dyes in response to the excitation beam generated by the laser 11 retraces the optical patn through the scanning mechanism 19, the prism 18, the steering mirror 17, to the dichroic beam splitter 16. The fluorescence comes from the focal point of the microscope objective 24 and is collimated with a diameter of about 8 millimeters as it comes out of the microscope objective. The dichroic beam splitter 16 allows the fluorescing wavelengths to proceed along path 26.

The beam on path 26 enters a bandpass filter 27, or a series of the same, which are designed to filter the backscattering of the laser beam itself which are due to weak reflections from the optical elements and surfaces of the capillary. These reflections may be much stronger than the actual fluorescence that is detected from the sample.

From the bandpass filters 27, a folding mirror 28 directs the beam through a focusing lens 29. The focusing lens brings the colimated light from the sample into a focus, and through a pinhole filter 30. The light from the capillary, which arises outside the focal point of the microscope objective 25 will not be columnated when it enters the lens 29. Thus the pinhole filter 30 rejects fluorescence from regions that are not of interest. The pinhole size is chosen so as to define a volume from which to collect fluorescence intensity from the sample. Typically, this volume is selected to be about five or ten times the expected volume of the target cells.

Through the pinhole 30, the beam enters a photomultiplier box 31. The photomultiplier box includes a dichroic beam splitter 32 which separates the detected fluorescence into two basic components. The first component, channel 0 is light having wavelengths below about 680 nanometers in the present embodiment. The second component channel 1, is light having wavelengths above about 680 nanometers Channel 0 is directed to a first photomultiplier 33. Channel 1 is directed to a second photomultiplier 34. Photomultipliers are connected across line 35 to the computer 40.

Also included in the mechanism, but not shown, is an autofocus mechanism. The autofocusing system uses an algorithm which involves measuring the fluorescence in a preliminary scan. At a first position in the capillary, the microscope objective focus is scanned to find the position of maximum fluorescence. This value is stored, and the objective is moved to a second position in the capillary. Again, focus in this position is scanned for maximum fluorescence. That value is stored. Using the two values, as a beginning and end point for the scan, the microscope focus is linearly extrapolated between the two to optimize the fluorescence reading along the length. In addition, the length of each scan line is set to be slightly larger than the width of the interior of the capillary. This is done to insure that every cell is detected by overscanning capillary dimensions, and later detecting the edges of the capillary to filter irrelevant information.

Fig. 2 schematically illustrates processing resources in the computer 40. The computer 40 includes a CPU 41 coupled through a system bus 42, as schematically illustrated. On the system bus 42 are a keyboard 43, a disk drive 44, or other non-volatile memory system, a display 45, and other peripherals 46, as known in the art. Also coupled to the bus 42 are a program memory 47 and a data memory 48. The output of the photomul-

tipliers, channel 0 and channel one, are supplied on lines 35-0 and 35-1, respectively, through analog to digital converters 49-0 and 49-1. The outputs of the analog to digital converters are 16 bit pixel values of the analog signals from channels 0 and 1. These values are supplied through a direct memory access (DMA) circuit 50 which transfers the pixel values into the data memory 48.

The processing system 40 includes resources that store scanned images of the data for channel 0 and 1, buffers used during the processing of the data, and memory for storing cell data once the cells or cell constituents are located, characterized and/or classified. Similarly, the program memory 47 includes resources for detecting the edges of the capillary, counting and locating target cells or cell constituents within the scanned images, characterizing the target cells or cell constituents, and reporting results. More details concerning the processing resources in the computer 40 are provided below with respect to the flow charts and graphs of Figs. 3-13. As will be appreciated, processing resources may be implemented with hardware, software, or a combination of both, as suits a particular use of the invention.

Fig. 3 illustrates the scanning technique used for gathering data from the capillary. The capillary 10, as illustrated in Fig. 3, has a width of about 0.667 millimeters, and a length of about 40 millimeters. A galvanometer scanning system scans the laser beam along a track 1 on a line longer than the capillary 10 is wide. At the end of line 1, the beam snaps back to the beginning of line 2 and scans line 2. The distance between the center of lines 1 and 2 is about 4 microns in the present embodiment.

For a capillary of about 0.667 millimeters in width, the scan lines are about 0.8 millimeters long. This provides 200 four micron samples along each scan line. For a 40 millimeter long capillary, with scan lines separated by 4 microns, about 10,000 scan lines are collected for each blood sample.

The analog to digital converters sample the scanned data at a rate which creates a pixel value representing fluorescence in a spot having dimensions of about 4 microns by 4 microns. Fig. 4 illustrates a 7X7 neighborhood of pixels. Thus, in the upper left hand corner pixel in row 1, column 1, is found. In the upper right hand corner, pixel in row 1, column 7, is found. In the center of the neighborhood of pixels, pixel row 4, column 4, is found. Similarly, in the lower right hand corner, pixel in row 7, column 7, is found. Fig. 4 also illustrates the size of the laser spot relative to the sample dimensions. In the preferred embodiment, the laser spot (e.g., 50) has a diameter of about 10 microns. Thus, oversampling occurs. That is, the laser spot 50 excites a region of 10 microns in diameter for the pixel at row 7, column 1. At row 6, column 1, a second spot 51 illuminates a region 10 microns in diameter which substantially overlaps with the spot 50 for row 7, column 1. Similarly, the spot 52 for row 7, column 2, substantially overlaps with the spot 50 and the spot 51 in column 1.

Fig. 5 illustrates a portion of a scanned image generated with one of the channels of the present invention. The graph of Fig. 5 is a baseline subtracted representation, where the baseline is illustrated at line 60. The baseline is essentially the average height of all the lines in the scan region. With this value subtracted, a number of peaks, e.g., peak 61, can be seen in the scanned image. These peaks typically correspond to target cells and are processed as described below. Also, each scan includes a region, generally 62, and a region, generally 63, which lie outside the capillary. The baseline 60 can be used to define the edges of the capillary because of the rapid falloff at 64 and 65 corresponding with the edges of the capillary. The processing resources characterizing the cells ignore pixel values outside the detected edges.

As mentioned above, there are two channels detected.

Fig. 5 illustrates a single channel. There will be a corresponding scanned image from the second channel having a similar profile, however, the amplitudes of the peaks will differ depending on the magnitude of the fluorescence detected in the second channel. Also, some peaks may be found in one image but not the other.

The basic data processing steps executed by the processing resources are illustrated in Figs. 6A and 6B. The first step in Fig. 6A is to receive the data from channel 0 and channel 1 (block 100). As the data is received, the DMA circuitry loads it into a buffer in the data memory (block 101). The buffer may be a circular buffer or other data structure used to keep track of the amount of data being received. The algorithm then determines whether a block of data having a prespecified size has been received (block 102). For the purposes of the present example, about 100 to 150 scan lines may comprise a suitable block size. If a block has not yet been completely received, then the algorithm determines whether the last block from a blood sample has been received (block 103). If it has, then the algorithm is done (block 104). If it has not, the algorithm loops into block 101 to continue loading data in the buffer.

When it is detected that a complete block has been received at block 102, then the algorithm parses the data into a plurality of scanned images by dividing the data into a raster image file Im0 for the first channel, and a raster image file Im1 for the second channel (block 105).

Data pre-processing involves reading in and processing the data in blocks. The signal processing requires signed numbers, thus, the unsigned 16 bit data is converted into 15 bit signed data.

Next, the two scanned images Im0 and Im1 are summed, or averaged, to generate a composite image Im2, and the composite image Im2 is stored (block 106).

Next, an edge detection algorithm, such as described below with respect to Fig. 11, is executed (block 107). The edge detection algorithm may be supplemented with an algorithm for evaluating the results to ensure that no false edges, such as might be detected by a bubble in a capillary, are found.

The edge detection is done using a baseline profile, where the baseline is the average of all the scans in the block, ignoring the scans that have peaks higher than a certain threshold.

After block 107, the algorithm proceeds to determine thresholds to be used for particle detection in the composite image Im2. These thresholds may be prespecified, empirically determined values, or they may be adaptively computed for each buffer or each sample. One algorithm for determining the threshold may involve determining the maximum and minimum values for each 7X7 pixel neighborhood in the block being processed. The maximum minus minimum value with the highest frequency of occurrence is used to estimate the threshold for particle detection. Distribution of the maximum and minimum for peaks of neighborhoods in the buffer are determined, and the thresholds are set so that peaks are detected if the maximum and minimum values in the neighborhood differ by amounts smaller than a threshold 3 standard deviations below the average peak height.

After determining the thresholds for particle detection in block 108, the algorithm proceeds to compute the background indices for the scanned images Im0 and Im1 using an algorithm such as described with respect to Fig. 10 (block 109). After computing the background indices, the algorithm may then proceed to do a baseline substraction step for the scanned images Im0 and Im1. This is an optional step, depending on the techniques used for particle detection and cell characterization set out below.

One baseline removal technique involves finding the minimum, or average of the N minimum lowest points along a given scan (N equal about 10). The above minimum, or average minimum, is then subtracted from all pixels in the block, and negative values are clipped to 0. Baseline removal is optional. In particular, if cell detection uses the peak slope criteria, as described below, it is not necessary to do baseline removal. However, it may be desirable to have baseline subtraction to eliminate edge effects in an overscanning situation.

After baseline subtraction for images Im0 and Im1, the algorithm does a particle detection routine using image Im2 (block 111). The particle detection process is illustrated below with respect to Fig. 12.

The next block determines whether a particle is detected (block 112). If a particle is detected, then the neighborhoods of pixels from images Im0, Im1 and optionally Im2 are saved, and cell parameters are computed using data in the neighborhood of the pixel maps, e.g. in response to the saved neighborhoods. If a particle is not detected, then the algorithm determines whether the Im2 buffer has been completely processed for particle detection (block 114). If not, the algorithm loops to block 111 to continue the particle detection routine. If the buffer has been finished, then the algorithm loops to block 102 in Fig. 6A, as illustrated, to begin processing a next block of data.

Thus, for example, the raw data consists of two 200xN (where N is less than or equal to 10,000) raster image files for each channel 0 and channel 1, where each pixel is a 16 bit unsigned integer, generated by the output of the analog to digital converters. The image data may be processed in blocks. Data for scan lines at the boundaries of the image block may be buffered to deal with cells crossing the image block boundaries.

The data block size is 200 pixels high by N scans wide, where N is about 128. The buffered block size may be 200 X 16 pixels on the block boundaries. By image processing in blocks, a smaller amount of memory resources are used for the image processing.

The technique of saving the neighborhood values from the scanned images for each block, as particles are detected, and then continuing to process additional blocks allows real time gathering of data and cell or cell constituent detection, with ability to compute cell parameters and characterize the cell later, or with a time shared processing technique. This greatly enhances the efficiency of use of the computation resources to allow sampling of very large amounts of scanned data in substantially real time.

Cell and cell constituent characterization, according to a preferred embodiment of the present invention, involves utilizing information from the two channels. The two channels in the present system include data which is relevant to both of the dyes which are to be detected. Thus, a technique must be used to discriminate information from the two dyes in the two channels that is efficient and noise immune. Accordingly, one embodiment of the present invention applies a linear regression technique over the neighborhoods of pixels saved for detected particles.

The problem to be solved can be appreciated with respect to Fig. 7, which schematically illustrates the spectra of fluorescence for the two dyes detected by channel 0 and channel 1, respectively. Thus, a cell containing antigens stained by the first dye will fluoresce with a spectrum such as spectrum 120. Similarly, the cell with a dye attached to an antigen of the second type will fluoresce with the spectrum 121. As can be seen, the two spectra substantially overlap. The dichroic beam splitter 32 in the photomultiplier mechanism 31, as shown in Fig. 1, splits the fluorescent beam along the 680 nanometer line 122 to generate two signals. This line has been empirically determined for the presently described system to provide good separation. Thus, the two signals both contain information which is generated in response to both dyes.

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The linear regression technique utilized to discriminate the information in the two channels is described with reference to Fig. 8. In particular, a 7X7 neighborhood of pixels is saved from each of image Im0 and Im1, centered on each target cell which is detected using the algorithm of Figs. 6A and 6B. The 49 coordinates may be plotted as shown in Fig. 8, where each dot is positioned with the magnitude of the first channel on axis X and the magnitude of the second channel along axis Y, such that sample at row 1, column 1, and sample at row 7, column 7, may appear at the points (1, 1) and (7, 7). Similarly, the sample at row 4, column 4, may appear at the point (4, 4). As can be seen, the sample from row 4, column 4, will have the highest average of amplitude from both channels because of the cell classification technique. The dots are then applied to a linear regression algorithm, as well known in the art, to find the best fit line 123 to the dot plot, Pres it al., Numerical Recipes in C, 1988, p. 523. This produces the slope "m" and the offset "a" for each target cell. Thus, the magnitude of the contribution from channel 0 can be expressed as the slope "m" times the magnitude of the contribution of channel 1, plus the offset value "a".

Fig. 9 is a graph which illustrates the technique used for characterizing the detected cells. In particular, the intensity value for a detected cell is defined as [CH1] for the scanned image Im1 and [Ch0] for the scanned image Im0 in the respective 7X7 neighborhoods. This intensity value is determined by a matched filtering technique based on the expected characteristics of target cells over the 7X7 neighborhoods.

A matched filter can be constructed from expected or typical pixel values in the neighborhood of a cell. The matched filter is a matrixl of coefficient which will be multiplied with the corresponding pixels from the neighborhood of the detected cell. The 49 resulting products can be summed to yield a single intensity value ([CH0] or [CH1]) for the detected cell. The coefficients can be chosen to sum to zero, in which case the constant background signal is cancelled out.

The intensity value for the cell is then plotted on the graph of Fig. 9 by multiplying the slope determined using the linear regression analysis above by the intensity value of one of the channels.

As can be seen, the graph of Fig. 9 is divided into five regions. The first region, 130, is for target cells which are dyed substantially only with the first dye which is centered on channel 1. The second region, 131, is defined for target cells which are dyed substantially only with the second dye. The third region 132 is defined for cells which are believed to be stained with both dyes. The fourth region 133 and the fifth region 135 are a "no call" region to ensure that bad data is ignored.

The first region 130 is defined during calibration of the device by doing a scan of a sample dyed only with the first dye. Linear regression analysis is applied to create a line 136 based on the one dye detection from channel 1. A similar technique is used to define line 137 for the second dye which has most of its spectrum detected by channel 0. A background index is calculated for the buffer in question to define regions indicated by dotted lines 138 and 139 below which for channel 1 and above which for channel 0, samples are characterized as having only one dye. The samples which fall in the region 132 are characterized as having both. Samples which fall in the regions 133 and 135, or which have a magnitude value which is too low, are characterized as no calls.

Appendix A provides a source code for the cell characterization routine according to one embodiment of the present invention as a means of providing an example of processing resources which might be used to accomplish this sort of classification.

The goal of cell or cell constituent classification is to determine the decision boundaries based on population-independent parameters. If necessary, the boundaries determined can be validated with population statistics.

In the CD3/CD4 assay, there are 3 cell populations present. The CD3 positive cells are stained with the Cy5 labeled antibody only. The CD4 cells are stained with both the Cy5 labeled CD3 antibody and the CyFr labeled CD4 antibody. The monocytes are stained with the CyFr labeled CD4 antibody only.

Since the CD3 positive cells and the monocytes are stained with one dye only, their slope distributions should cluster around the Cy5 and CyFr slopes respectively. The Cy5 and CyFr slopes are determined in the compensation matrix calibration. The spread or distribution of the clusters can be determined from the background noise estimates.

Similarly, in the CD3/CD8 assay, there are 3 cell populations present. The CD3 positive cells are stained with the Cy5 labeled antibody only. The CD8 cells are stained with both the Cy5 labeled CD3 antibody and the CyFr labeled CD8 antibody. The NK cells are stained with the CyFr labeled CD8 antibody only.

Since the CD3 positive cells and the NK cells are stained with one dye only, their slope distributions should cluster around the Cy5 and CyFr slopes respectively. The Cy5 and CyFr slopes are determined in the compensation matrix calibration. The spread or distribution of the clusters can be determined from the background noise estimates.

The following classification rules may be applied:

Non-Cells

A particle is classified as non-cell, if any of the following criteria is met:
1. Particles with correlation coefficient (for the regression fit for planes 0 and 1) less than the threshold value (0.8).
2. Channel 0 value less than background noise threshold.
3. Channel 1 value less than background noise threshold.

Monocytes and NK Cells

1. Cells with channel 1 value greater than the CyFr slope line minus a constant background noise offset for channel 1.

CD3 Cells

1. Cells with channel 1 value less than the Cy5 slope line plus a constant background noise offset for channel 1.

CD4/8 Cells

Any cell that does not satisfy the above criteria are potentially a CD4/8 cell. Cells that lie too close to the Cy5 or CyFr slopes are labeled as "no-calls". The slopes difference between the CyFr and Cy5 slope are divided into slope regions. Cells that are below the 10% or above the 90% region boundaries are classified as no-calls.

The use of the slope value from the linear regression analysis provides a noise immunity, and improves the robustness of the system. This analysis may be replaced by solving two equations with two unknowns based on the intensity values for channel 0 and channel 1, respectively.

The cross correlation coefficient between corresponding pixels from image 0 and image 1 is determined. If the signal is dominated random noise, one would expect a poor correlation coefficient. A cell with good signal gives a correlation that ranges from 0.9 to 1.0.

The cross-correlation technique can be extended to correlate individual cells with the average cell profile. A composite average cell profile can be generated by averaging the cell profile of all the cells detected. A good correlation coefficient indicates that the cell shape is similar to the average cell shape. An artifact peak usually has a different cell shape profile and thus gives a poorer cross correlation coefficient.

Fig. 10 illustrates an algorithm for computation of the background noise indices, used as described above, with respect to Fig. 9, to define the regions around the line for the two dyes within which a cell will be characterized as containing only that dye.

This background index can be computed for each buffer, or it can be computed across the entire image.

The technique involves defining a plurality of bins for N background baseline noise levels, where N is about 2,000, and each bin 16 bits wide, in one embodiment (block 200). For each buffer a WXW pixel map surrounding each pixel is defined, such that WXW is large enough to contain almost all the signal from the expected size of the cell. This may be about 5X5 in the present example (block 201).

For each WXW pixel map, the maximum and minimum pixel values are determined for each pixel in images Im1 and Im0 (block 202).

Each pixel is then assigned an integer bin number based on the difference between the maximum and minimum values within the pixel map divided by the size of the allocated bins (block 203). As mentioned above, there may be 2,000 bins, 16 bits wide each for a range of about 32,000 values.

With the integer bin number, the count for the corresponding bin is incremented for that pixel (block 204). After incrementing the bin number, the algorithm determines whether there are more pixels to process for the buffer (block 205). If there are, it loops back to block 201. If not, the algorithm determines the bin number with the highest count (block 206). The background noise index for this buffer is set to the bin number with the highest occurrence times the bin size (block 207). These indices are then stored for both channels (block 208). As mentioned above, the process is carried out for both channels to achieve two separate background noise indices.

Fig. 11 illustrates an algorithm for performing edge detection, as mentioned above. Because the blood sample in this example will contain free dye labelled antibody, a distinct background signal results. This signal is used to locate the boundary of the lumen of the capillary. The average image Im2 from channel 0 and channel 1 is generated (block 300). A specified number N of scans are averaged pixel by pixel to produce an average

scan (block 301). The maximum and minimum values are determined from the average scan (block 302). Next, a threshold is set based on the difference between the maximum and the minimum times a factor which ranges from 0.1 to 0.8 (block 303). This establishes a threshold which is a percentage of the average amplitude of fluorescence from a given scan line. The scan lines are then searched from center of the scan to the left until the baseline value is less than the threshold for left edge detection. The left edge is then set as the location where the threshold is crossed (block 304). Similarly, the algorithm searches from the center of the scan to the right until the threshold for right edge detection is passed. The location of the right edge is then defined as the location where the threshold is crossed (block 305). Using edge detection, scanned pixels outside of the detected edges are ignored in the additional processing described above.

Fig. 12 illustrates the algorithm for detecting a cell or cell constituent. The cell detection algorithm uses the image Im2, which is based on the average (or sum which for this purpose is substantially the same thing) of images Im0 and Im1 (block 400). A 5X5 pixel map surrounding each pixel is then defined in sequence (block 401). This pixel map is tested. The test is a five step test which involves determining whether the center pixel is the pixel having the highest value of all pixels in the pixel map. If it is, then the test takes the difference between the center pixel and the top left corner pixel and determines whether this difference is greater than a threshold which is assigned for cell or cell constituent detection. Next, the center pixel and the top right corner are used to make the threshold determination. Next, the center pixel and the bottom left corner pixel are used to make the threshold determination. Next, the center pixel and the bottom right corner pixel are used to maker the threshold determination. If the center pixel has the highest value, and another pixel in the map has an equal value, then the algorithm passes the test. In order to avoid counting a cell twice, in this instance, the center pixel value is incremented by one, so that when the other pixel value having the high value is encountered, it will be determined that it is not the highest value pixel (block 402).

If all five conditions have been satisfied (block 403), the x and y coordinate for the center pixel is saved, and a 7X7 pixel map, or neighborhood, surrounding the center pixel is saved from each image Im0 and Im1 in the cell parameter list (block 404). These values can be used for later processing of the data as described above.

Using the averaged (or summed) image for cell detection provides better cell resolution, because of magnitude of the signal from any one of the two dyes may be very low on a given cell. This cell or cell constituent detection is based on the maximum an minimum values in the neighborhood around the detected cell, rather than an absolute peak value. This provides immunity from background levels may vary over the scanned region.

Fig. 13 illustrates the basic algorithm for linear regression analysis of the 7X7 pixel map. The linear regression analysis begins by taking the 7X7 pixel map of a detected cell from both images I0 and I1 (block 500). A linear regression line is fitted for corresponding pixel points from images Im0 and Im1 over the indices for the row i and the column j, such that Im1 (i.j) approximates to the slope times Im0 (i.j) plus an offset (block 501). After fitting the regression line, the slope offset and correlation coefficient r2 (goodness of fit) are stored in the cell parameter list (block 502).

Thus, a linear regression line fit is computed between the corresponding pixels from image 0 and image 1 and the slope and goodness of fit values are obtained. The slope determined indicates whether the cell is stained with 1 of 2 antibodies. Using a 7X7 pixel map to determine the slope gives a better estimate of the slope of the cell. The goodness of fit indicates the goodness of the data. The advantages of the linear regression analysis include noise reduction, a good estimate of signal quality, a system insensitive to baseline subtraction and the well defined orthogonal coordinates.

In sum, a method and apparatus is provided for processing data generated by one or more channels of data, where the channels include information relevant to more than one characteristic to be determined and are taken from a container. The technique allows for counting and characterizing the cells or cell constituents within the contained region with minimum operator handling of the samples, repeatability, and efficient utilization of processing resources.

The data processing resources accomplish data collection, image averaging for capillary edge and cell detection operations background noise determination, baseline removal, and cell characterization.

The data from a detected cell or cell constituent is then extracted by saving it into a cell parameter list in memory. This allows continuous scans of large volumes of data, with processing of the data saved for later steps when more processing resources may be available. Also, it allows reanalysis of data for detected cells in the future based on much reduced file sizes, as compared to what would result if the entire 200 by 10,000 pixel file must be saved for later analysis.

The described embodiment provides a system for processing scanned data which is very robust and accurate. It allows concurrent data collection and analysis, as well as analysis of data after collection. Further, it allows for completion of data analysis very rapidly, shortly after completion of the data collection systems.

The foregoing description of a preferred embodiment of the invention has been presented for purposes of illustration and description. It is not intended to be exhaustive or to limit the invention to the precise forms disclosed. Obviously, many modifications and variations will be apparent to practitioners skilled in this art. It is intended that the scope of the invention be defined by the following claims and their equivalents.

APPENDIX A

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SOURCE CODE FOR CELL CHARACTERIZATION

```
const float kCellCorrelationCoefThreshold = 0.8;

CELL-TYPE CCell::CellClassification( )
{
        float    maxSlope = CyFrSlope - ((CyFrSlope-CySSlope) * 0.1);
        float    minSlope = Cy5Slope + ((CyFrSlope-Cy5Slope) * 0.1);

        if ( (cellCorrelationCoef < kCellCorrelationCoefThreshold) ||
             (peakValue0 < noiseThreshold0) ||
             (peakValue1 < noiseThreshold1) )
             return (NON_CELL);                        // noise peak
        else if ( (peakValue1 > (CyFrSlope * peakValue0 + noiseLevel) )
             return (CYFR_POSITIVE);          //monocyte or NK cells
        else if ( peakValue1 < (Cy5Slope * peakValue0 + noiseLevel) )
             return(CYS_POSITIVE);            //CD3 cells
        else if ( (cellSlope > maxSlope) || (cellSlope < minSlope) )
             return (NO_CALL);                // No call
        else
             return (CYFR_CYF_POSITIVE); //        CD4/8 cell
}
```

Claims

1. An apparatus for analysis of a sample of cells or cell constituents, the cells or cell constituents having detectable characteristics; comprising: a scanner which scans the sample to generate a channel of data containing information relevant to the detectable characteristics; sampling circuitry, which samples the channel of data to generate a stream of pixel values for a scanned image of the sample; a processing system having memory and coupled to the sampling circuitry, including resources which load the stream of pixel values into a pixel map buffer in the memory, analyse the pixel map buffer to identify certain cells or cell constituents in the scanned image, and save a neighbourhood of pixel values for each identified cell or cell constituent for later processing.

2. An apparatus for analysis of a sample of cells or cell constituents having detectable characteristics; comprising: a container having detectable edges and a lumen for the sample; a scanner which scans the container to generate a channel of data containing information relevant to the detectable characteristics of the sample in the lumen of the container;
    sampling circuitry, which samples the channel of data to generate a stream of pixel values for a

scanned image of the sample;

a processing system having memory and coupled to the sampling circuitry, including resources which load the stream of pixel values into a pixel map buffer in the memory, analyse the pixel map buffer to detect edges of the lumen, and analyse the pixel map buffer to identify certain cells or cell constituents while ignoring pixel values in the scanned image outside the detected edges of the lumen.

3. The apparatus of claim 2, wherein the processing system includes resources to save a neighbourhood of pixel values for each identified cell or cell constituient for later processing.

4. The apparatus of claim 1 or claim 2, wherein the scanner generates two channels of data, and the sampling circuitry generates two streams of pixel values for respective scanned images of the sample, and wherein the resources of the processing system save a neighbourhood of pixel values from both scanned images for each identified cell or cell constituient for later processing.

5. The apparatus of claim 4, wherein the processing system includes resources for characterizing the identified cells or cell constituents using information in the neighbourhoods of pixel values saved from both scanned images.

6. The apparatus of claim 5, wherein the resources for characterizing perform linear regression analysis of corresponding pixel values from the two neighbourhoods saved for a particular identified cell or cell constituient.

7. The apparatus of claim 1 or claim 2, wherein the processing system includes resources for characterizing the identified cells or cell constituents using information in the neighbourhood of pixel values saved from the scanned image.

8. An apparatus for analysis of a sample of cells or cell constituents, the cells or cell constituents having detectable characteristics; comprising: a scanner which scans the sample to generate a channel of data containing information relevant to the detectable characteristics; sampling circuitry, which samples the channel of data to generate a stream of pixel values for a scanned image of the sample; a processing system having memory and coupled to the sampling circuitry, including resources which load the stream of pixel values into a pixel map buffer in the memory, analyse the pixel map buffer to identify certain cells or cell constituents in the scanned image, and save a set of cell or cell constituient parameters calculated from the pixel values.

9. The apparatus of claim 8, wherein the scanner generates two channels of data, and the sampling circuitry generates two streams of pixel values for respective scanned images of the sample, and wherein the resources of the processing system save a set of cell or cell constituient values from both scanned images for each identified cell or cell constituient for later processing.

10. The apparatus of claim 8, wherein the processing system includes resources for characterizing the identified cells or cell constituents using information in the sets of parameters of pixel values saved from both scanned images.

11. The apparatus of claim 10, wherein the resources for characterizing perform linear regression analysis of corresponding pixel values from the two sets of parameters saved for a particular identified cell or cell constituient.

12. The apparatus of claim 8, wherein the processing system includes resources for characterizing the identified cells or cell constituents using information in the set of parameters of pixel values saved from the scanned image.

13. The apparatus of claim 1 or claim 8, wherein the resources which analyse the pixel map buffer to identify certain cells or cell constituents in the scanned image, include resources for detecting edges of the sample and ignoring pixel values outside the detected edges.

14. The apparatus of claim 4 or claim 9, wherein the resources which identify certain cells or cell constituents are responsive to the two streams of pixel data.

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15. The apparatus of claim 7 or claim 12, wherein the resources for characterizing the identified cells or cell constituents include a filter based upon an expected characteristic of the cells or cell constituents, and resources responsive to the filter to generate an intensity value for the identified cell or cell constituient.

16. The apparatus of claim 15, wherein the resources for characterizing the identified cell or cell constituient include resources responsive to the filter to generate an intensity value for the identified cell or cell constituient, independent of other saved pixel values.

17. The apparatus of any of claims 1, 2 or 8, wherein the cells are blood cells.

18. The apparatus of claim 17, wherein the cells are labelled with a fluorophore excitable in the range of 600 to 1000 nm.

19. A method for analyzing a sample of cells or cell constituents having a plurality of detectable characteristics in a container, comprising: scanning the container with a detector to generate a plurality of channels of data, at least one particular channel containing information relevant to more than one of the plurality of detectable characteristics; sampling the plurality of channels of data to produce a corresponding plurality of scanned images of the sample; and analyzing the plurality of scanned images to characterize the certain cells or cell constituents in response to the plurality of channels of data, including processing the scanned image corresponding to the at least one particular channel to distinguish the more than one of the detectable characteristics.

20. The method of claim 19, wherein the step of analyzing the plurality of scanned images includes the step of processing at least one of the plurality of scanned images to identify segments of the plurality of scanned images containing certain cells or cell constituents.

21. The method of claim 19, wherein the step of processing the scanned image corresponding to the at least one particular channel includes using another one of the plurality of scanned images in combination to distinguish the more than one of the detectable characteristics.

22. The method of claim 21, wherein the step of using another one of the plurality of scanned images in combination includes performing a linear regression analysis based upon corresponding portions in the at least one particular scanned image and the another one of the plurality of scanned images, to determine a slope value indicating relative contributions of the more than one of the detectable characteristics.

23. The method of claim 19, wherein the container has detectable edges, and at least one of the channels of data includes information relevant to the edges of the container, and including processing at least one of the scanned images to detect the edges of the container; and wherein the step of analyzing the plurality of scanned images to characterize the certain cell or cell constituent includes ignoring pixels in the scanned image outside the detected edges of the container.

24. The method of claim 19, wherein the cells are blood cells.

25. The method of claim 19, wherein the cells are labelled with a fluorophore excitable in the 600 to 1000 nm range.

26. A method for analyzing a sample of cells or cell constituents having two detectable characteristics, comprising: scanning the sample with a detector to generate two channels of data, each channel containing information relevant to the two of detectable characteristics; sampling the two channels of data to produce a corresponding plurality of scanned images of the sample; and analyzing the two scanned images to characterize the certain cells or cell constituents in response to the two channels of data, including performing a linear regression analysis over corresponding portions in the two scanned images.

27. The method of claim 26, wherein the step of analyzing the two scanned images includes the step of processing at least one of the two scanned images to identify segments of the two scanned images containing certain cells or cell constituents, and wherein the linear regression analysis is performed over the identified segments.

28. The method of claim 20 or claim 27, including filtering the identified segments based upon expected characteristics of the certain cells or cell constituents to generate respective intensity values for the identified segments.

29. A method for analyzing in a container with detectable edges a sample of cells or cell constituents having detectable characteristics, comprising: scanning the container with a detector to generate a channel of data containing information relevant to the detectable characteristics and the edges of the container; sampling the channel of data to produce a scanned image of the container; and processing the scanned image to detect the edges of the container; and analyzing the scanned image to characterize the certain cells or cell constituents in response to the channels of data, including ignoring portions in the scanned image outside the detected edges of the container.

30. The method of claim 29, wherein the step of analyzing the scanned image includes the step of processing the scanned image to identify segments of the scanned image containing certain cells or cell constituents.

31. The method of claim 30, including filtering portions within the identified segments based upon expected characteristics of the certain cells or cell constituents to generate respective intensity values for certain cells or cell constituents within identified segments.

32. The method of claim 30, including defining a neighbourhood of pixels for each identified segment, the neighbourhood being larger than an expected size of a certain cell; and processing the pixels within the neighbourhood to compensate for background signal and generate an intensity value for the certain cell within the neighbourhood.

33. The method of claim 32, wherein the step of processing the pixels within the neighbourhood includes filtering pixels within the neighbourhood based upon an expected shape of the certain cells to generate an intensity value for a certain cell within the neighbourhood.

34. A method for analyzing a sample of cells or cell constituents with detectable characteristics in a container having edges, comprising: scanning the container with a detector to generate a channel of data containing information relevant to the detectable characteristics and the edges of the container; sampling the channel of data to produce a scanned image of the container; processing the scanned image to identify segments of the scanned image containing certain cells or cell constituents; and filtering portions within the identified segments based upon expected characteristics of the certain cells or cell constituents to generate respective intensity values for certain cells or cell constituents within identified segments.

35. The method of claim 34, wherein the step of filtering includes defining a neighbourhood of pixels for each identified segment, the neighbourhood being larger than an expected size of a certain cell; and processing the pixels within the neighbourhood to compensate for background signal and generate an intensity value for the certain cell or cell constituent within the neighbourhood.

36. The method of claim 35, wherein the step of processing the pixels within the neighbourhood includes filtering portions within the neighbourhood based upon an expected shape of the certain cells or cell constituents to generate an intensity value for a certain cell or cell constituent within the neighbourhood.

37. A method for analysing a sample of cells or cell constituents, the cells or cell constituents having detectable characteristics, comprising: scanning the sample with a detector to generate a channel of data containing information relevant to the detectable characteristics; sampling the channel of data to produce a scanned image of the sample; processing the scanned image to identify segments of the scanned image containing certain cells or cell constituents; defining a neighbourhood of pixels for each identified segment, the neighbourhood being larger than an expected size of a certain cell; and saving the neighbourhood of pixels defined for each identified segment, for further processing.

38. A method for analyzing a sample of cells or cell constituents, the cells or cell constituents having detectable characteristics, comprising: scanning the sample with a detector to generate a channel of data containing information relevant to the detectable characteristics; sampling the channel of data to produce a scanned image of the sample; processing the scanned image to identify segments of the scanned image containing certain cells or cell constituents; defining a neighbourhood of pixels for each identified seg-

ment, the neighbourhood being larger than an expected size of a certain cell or cell constituent; and saving a set of cell or cell constituent parameters calculated from the neighbourhood of pixels defined for each identified segment, for further processing.

39. The method of claim 37 or claim 38, wherein the further processing comprises: processing the pixels within the neighbourhood to compensate for background signal and generate an intensity value for the certain cell or cell constituent within the neighbourhood.

40. The method of claim 39, wherein the step of processing the pixels within the neighbourhood includes filtering pixels within the neighbourhood based upon an expected shape of the certain cells or cell constituent and background intensity to generate an intensity value for a certain cell or cell constituent.
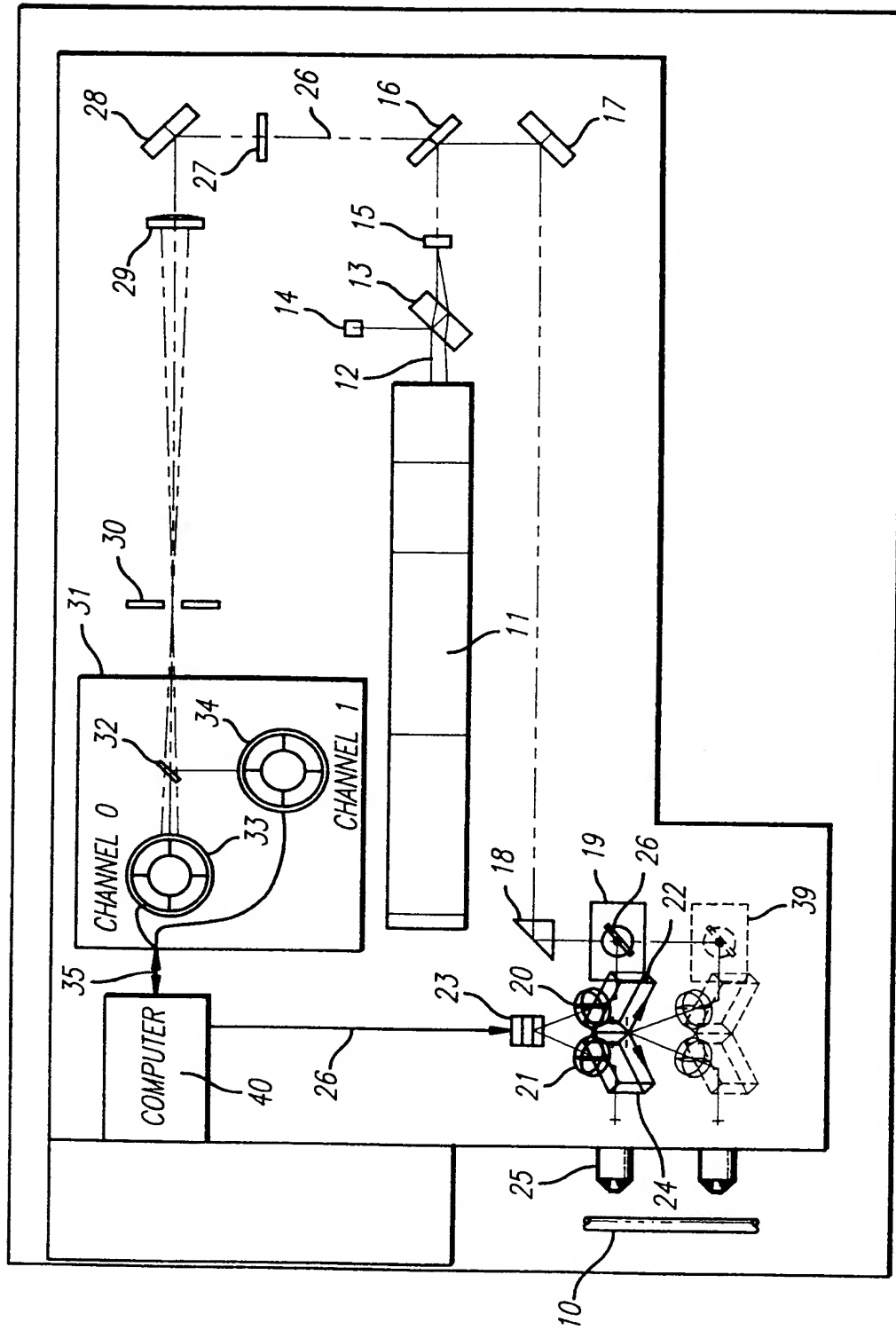
FIG. 1
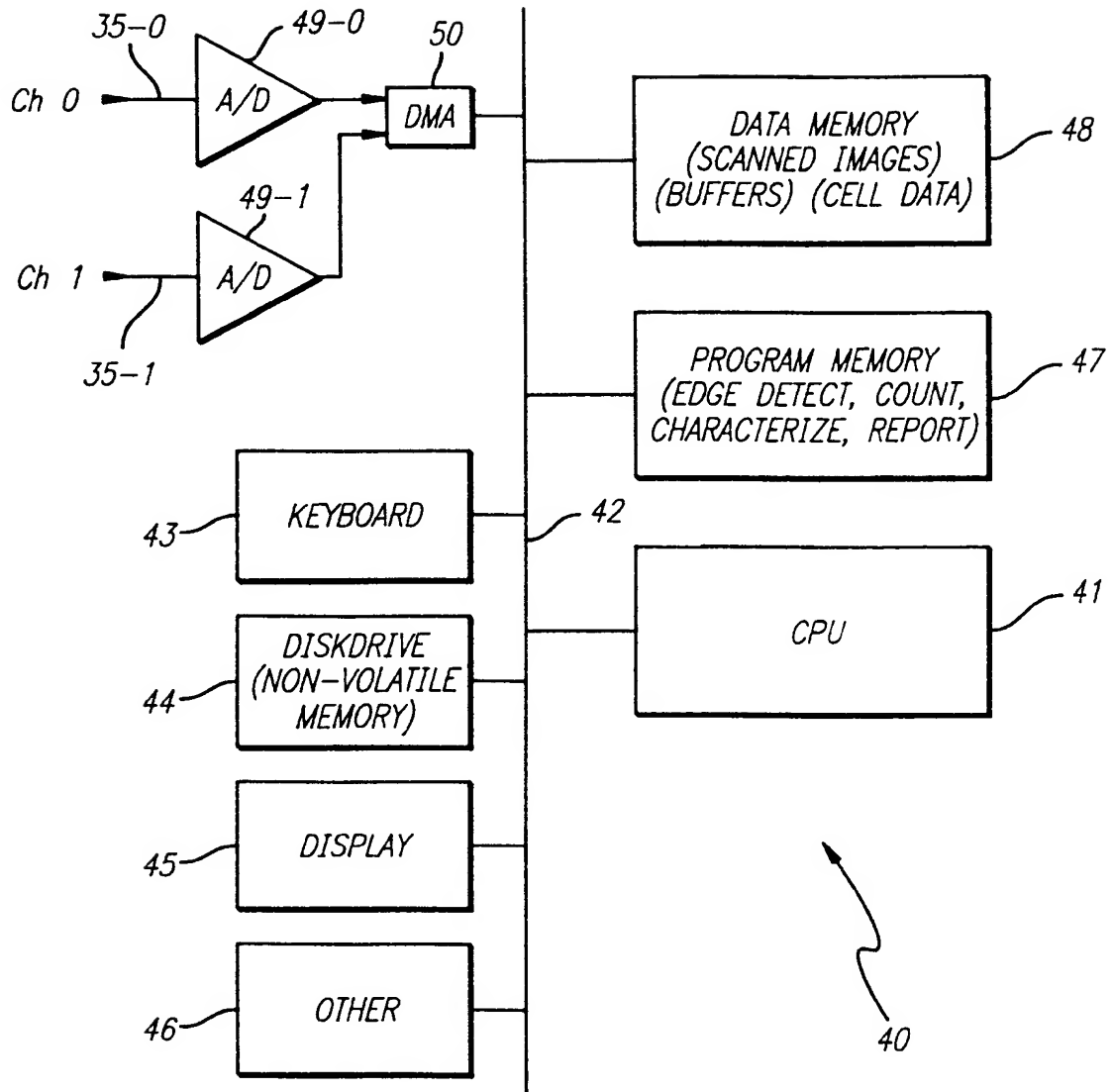
FIG. 2

FIG. 3

FIG. 4

FIG. 5

(BASELINE SUBTRACTED)

FIG. 6A

100 — RECEIVE DATA FROM CHANNEL 0 AND CHANNEL 1

101 — LOAD IN BUFFER (CIRCULAR)

← FROM FIG. 6B

103

LAST BLOCK ?

NO

BLOCK RECEIVED ?

NO

102

YES

104 — DONE

YES

PARSE DATA INTO Im0 AND Im1 BUFFERS — 105

SUM Im0 AND Im1 EQUAL Im2, STORE Im2 — 106

DO EDGE DETECTION ON Im2 (WITH BUBBLE DETECTION) BASELINE PROFILE — 107

FIG. 6B

108 — DETERMINE THRESHOLD(S)
FOR PARTICLE
DETECTION IN Im2

109 — COMPUTE BACKGROUND
INDICES FOR Im0 AND Im1

100 — DO BASELINE
SUBTRACTION IN
Im0 AND Im1

111 — DO PARTICLE
DETECTION IN
Im2

112 — PARTICLE
DETECTED
?

NO

114 — FINISHED WITH
Im2 BUFFER
?

NO

YES

TO
FIG. 6B

YES

113 — SAVE NEIGHBORHOOD,
COMPUTE CELL
PARAMETERS
Im0; Im1

FIG. 7

$$ChO = m(Ch1) + a$$

FIG. 8

FIG. 9

FIG. 10 | BACKGROUND NOISE INDICES FOR IMAGE 0 AND 1 |

200 —— | FOR EACH IMAGE ALLOCATE BINS FOR N BACKGROUND BASELINE NOISE LEVELS |

NEXT PIXEL

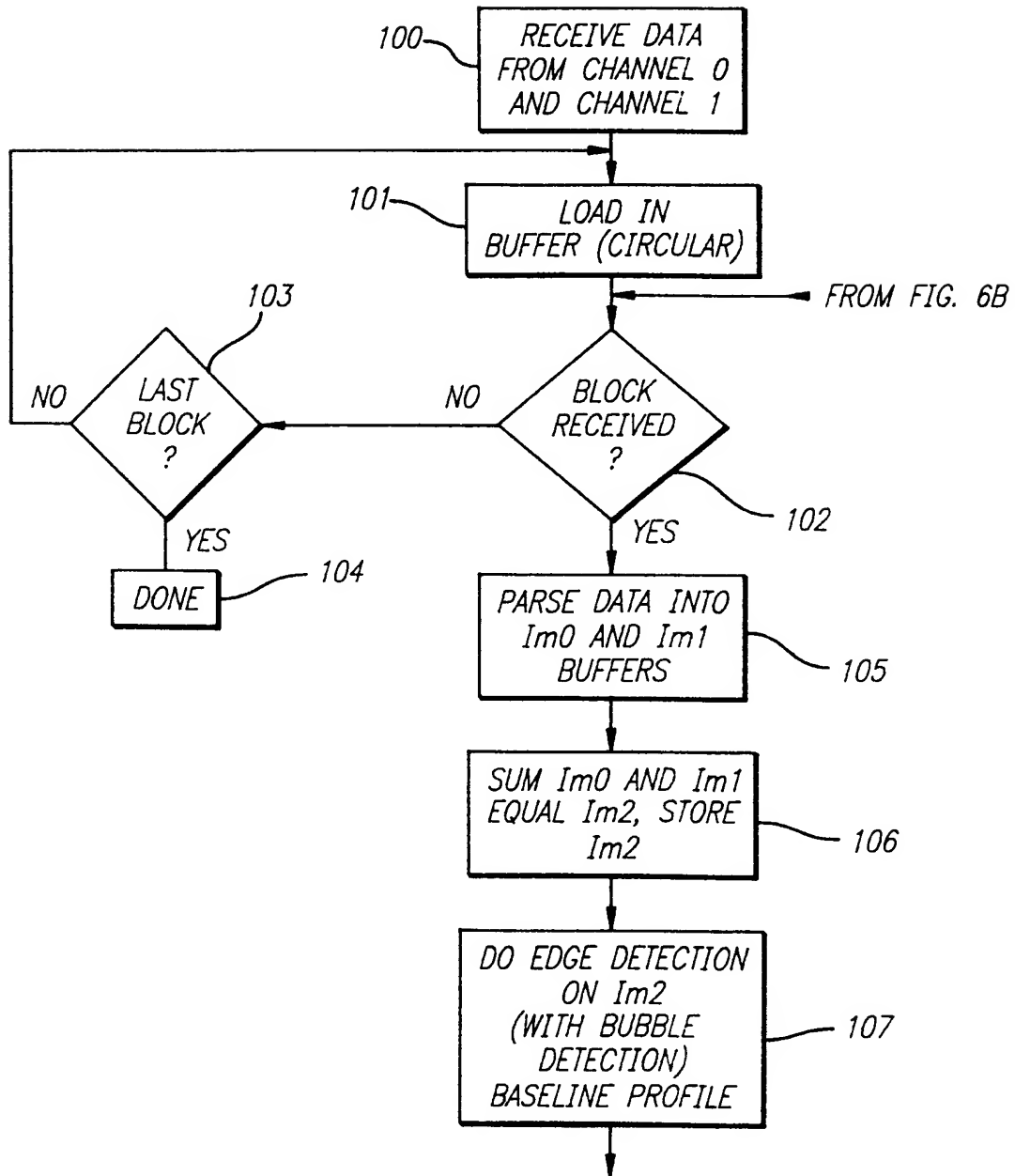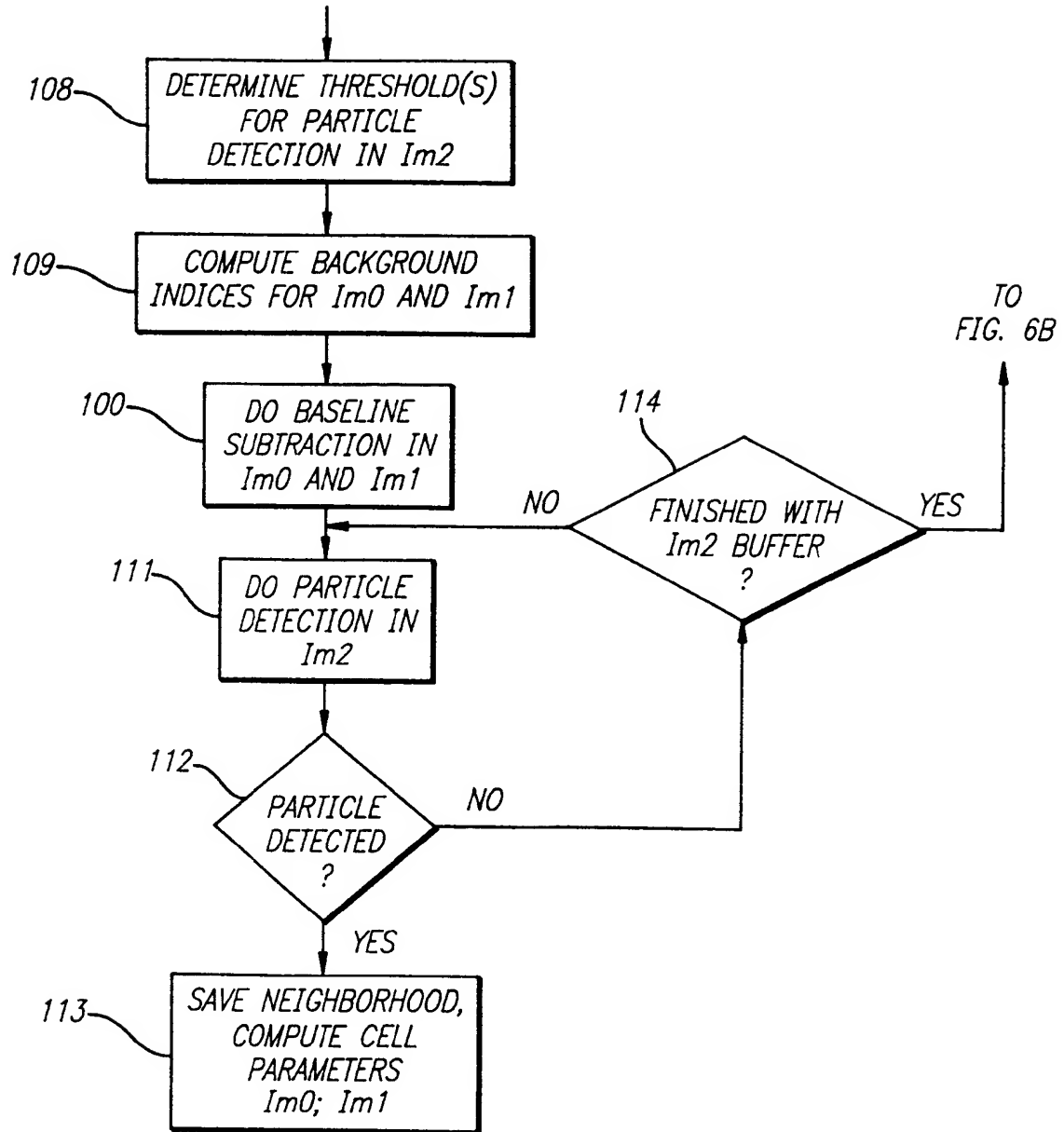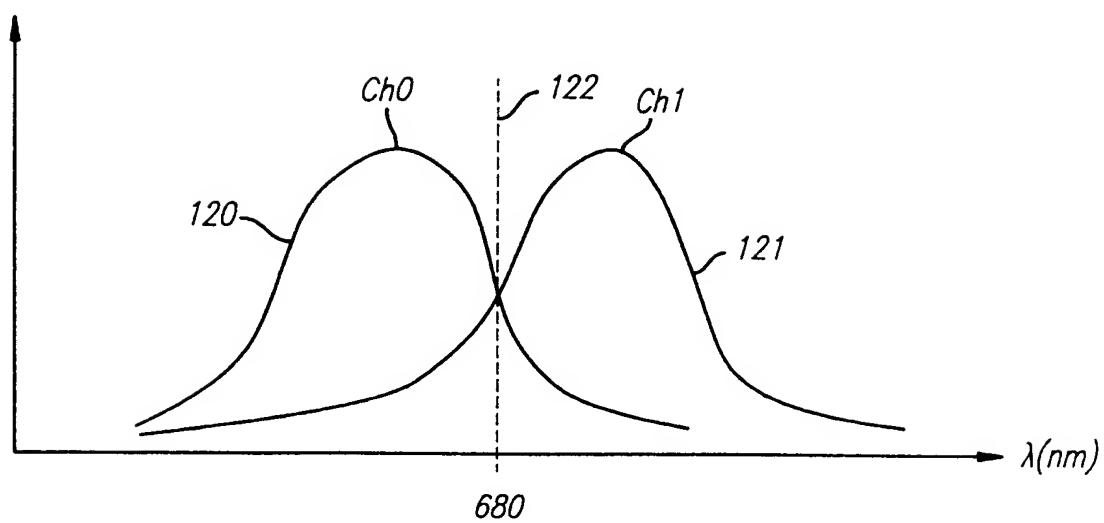| DEFINE A WXW PIXEL MAP/SURROUNDING EACH PIXEL (WXW LARGE ENOUGH TO CONTAIN ALMOST ALL THE SIGNAL FROM THE CELL | — 201

| FIND THE MAXIMUM AND MINIMUM PIXEL VALUES FROM THE WXW PIXEL MAP FROM IMAGES 0 AND 1 | — 202

203

| BIN NUMBER = (MAXIMUM − MINIMUM) / BIN SIZE |

| ADD 1 COUNT TO CORRESPONDING BIN FOR THE BIN NUMBER | — 204

YES | MORE PIXEL TO PROCESS ? | — 205

NO

206 — | FIND BIN NUMBER WITH THE HIGHEST OCCURRENCE (HBN) |

207 — | BACKGROUND NOISE INDEX = BIN NUMBER WITH THE HIGHEST OCCURRENCE * BIN SIZE |

208 — | STORE BACKGROUND NOISE INDICES FOR CHANNEL 0 AND 1 |

FIG. 11

EDGE DETECTION

GENERATE
AVERAGE IMAGE
FROM CHANNEL 0
AND 1 IMAGES   — 300

AVERAGE N SCANS IN
THE X DIRECTION   — 301

FIND
MAXIMUM AND
MINIMUM FROM
AVERAGE SCAN   — 302

THRESHOLD = (MAXIMUM —
MINIMUM) * FACTOR
FACTOR RANGES FROM 0.1 TO 0.8   — 303

SEARCH LEFT FROM CENTER OF SCAN
TILL BASELINE VALUE < THRESHOLD
LEFT EDGE LOCATION = LOCATION
WHERE ABOVE CONDITION FIRST
OCCURS   — 304

SEARCH RIGHT FROM CENTER OF SCAN
TILL BASELINE VALUE < THRESHOLD
RIGHT EDGE LOCATION = LOCATION
WHERE ABOVE CONDITION FIRST
OCCURS   — 305

FIG. 12

CELL DETECTION

USING AVERAGE IMAGE FROM IMAGE 0 AND1 — 400

SELECT 5X5 PIXEL MAP SURROUNDING EACH PIXEL — 401

TEST
1. (CENTER PIXEL − TOP LEFT CORNER PIXEL) > THRESHOLD
2. (CENTER PIXEL − TOP RIGHT CORNER PIXEL) > THRESHOLD
3. (CENTER PIXEL − BOTTOM LEFT CORNER PIXEL) > THRESHOLD
4. (CENTER PIXEL − BOTTOM RIGHT CORNER PIXEL) > THRESHOLD
5. CENTER PIXEL > ALL THE PIXEL IN THE 5X5 PIXEL MAP
— 402

ALL FIVE CONDITIONS ABOVE SATISFIED — 403

SAVE X, Y, COORDINATE FOR CENTER PIXEL AND 7X7 PIXEL MAP SURROUNDING THE CENTER PIXEL FROM IMAGE 0 AND 1 IN CELL PARAMETER LIST — 404

FIG. 13

REGRESSION
ANALYSIS

7X7 PIXEL
MAP OF CELL
FROM IMAGES
0 AND 1 — 500

FIT LINEAR REGRESSION LINE TO CORRESPONDING PIXEL POINTS FROM
IMAGES 0 AND 1 — 501
IMAGE1(i,j) = SLOPE * IMAGE0(i,j) + OFFSET

STORE THE SLOPE, OFFSET AND CORRELATION
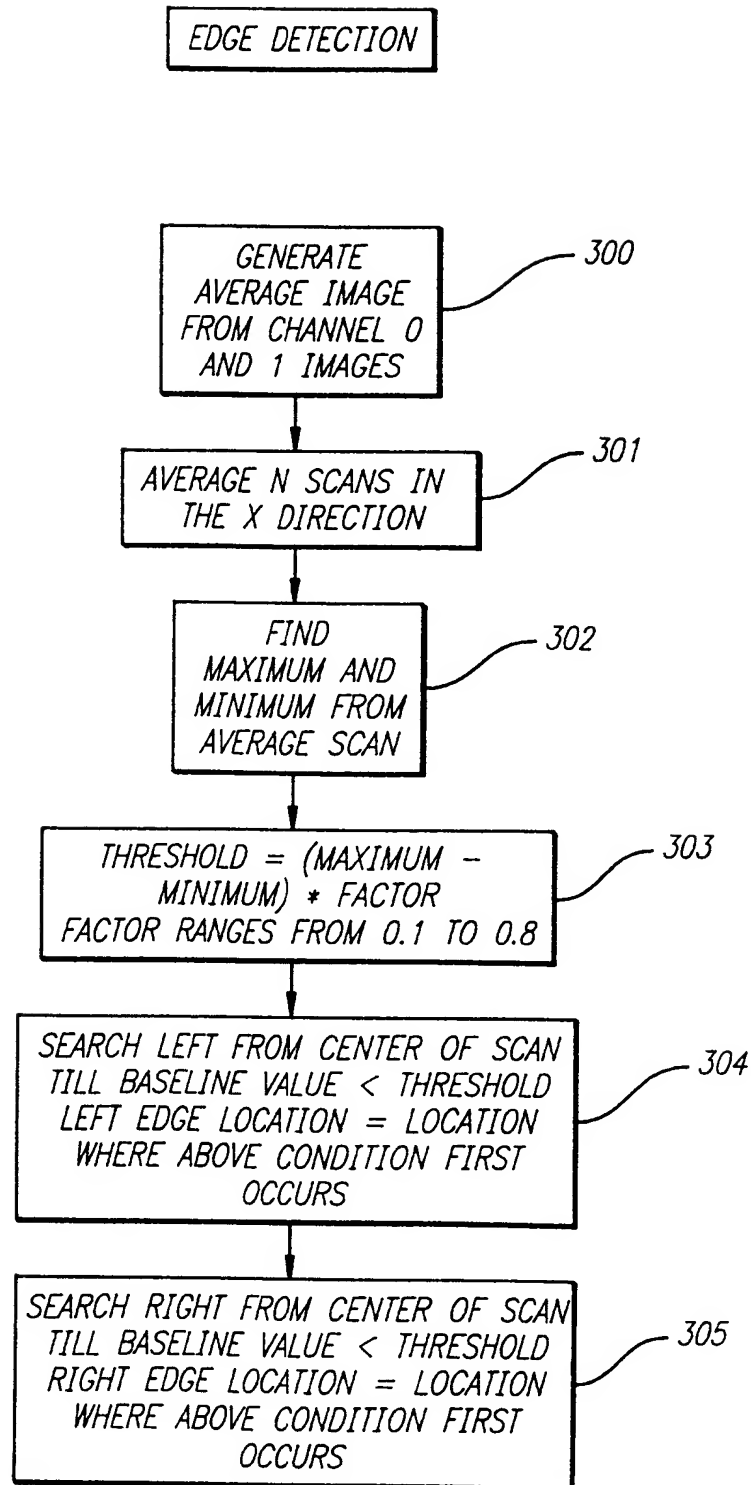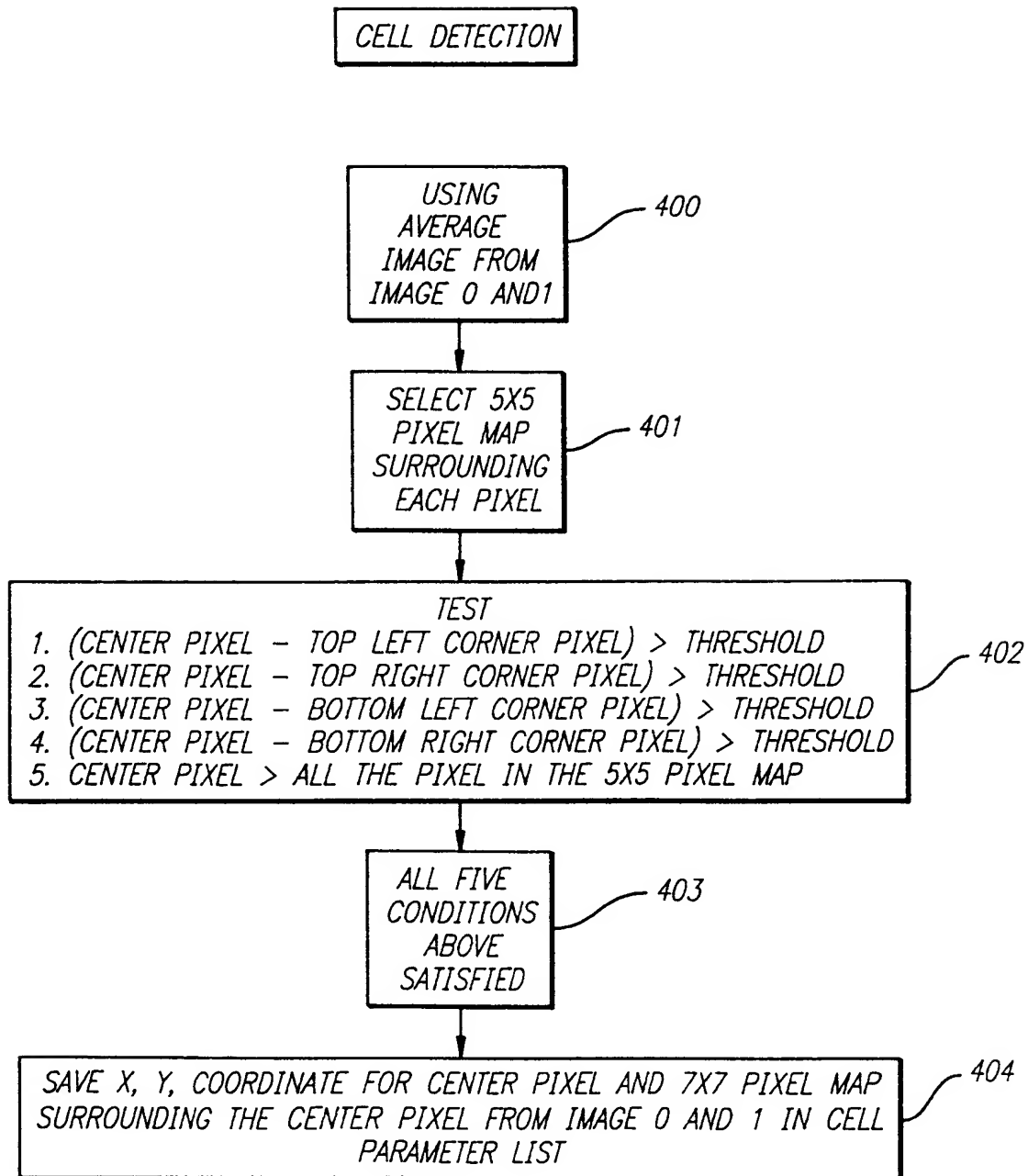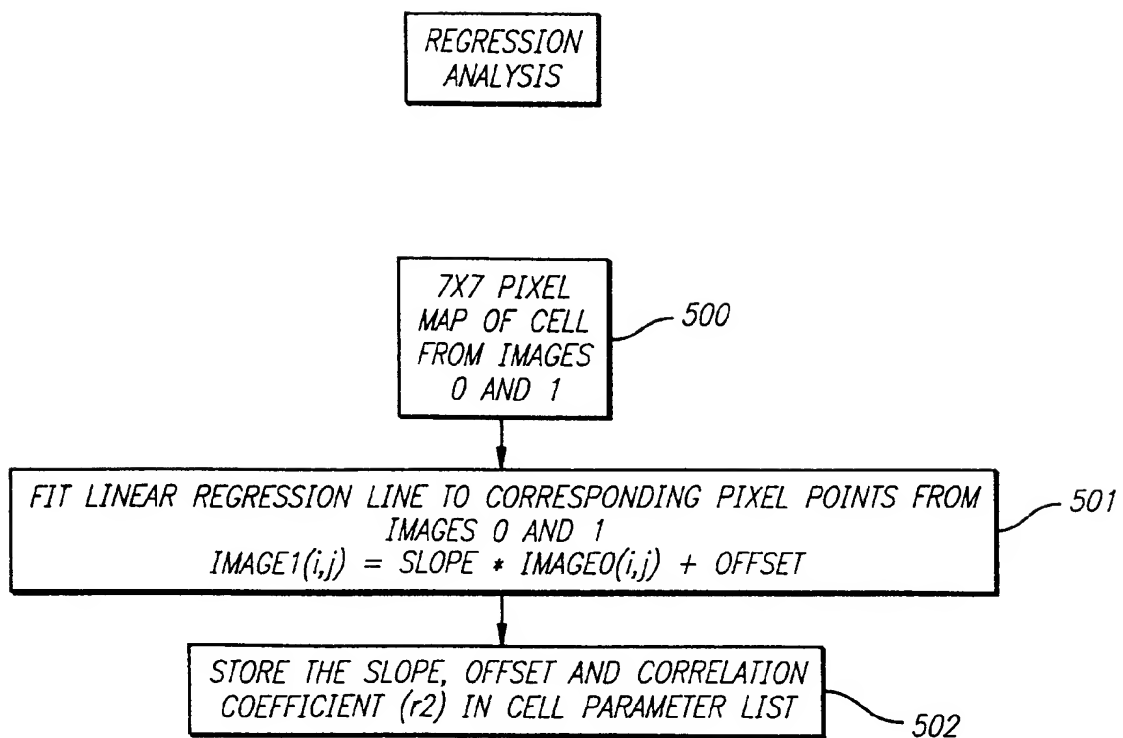COEFFICIENT (r2) IN CELL PARAMETER LIST
— 502

European Patent Office

EUROPEAN SEARCH REPORT

Application Number

EP 95 30 2975

DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document with indication, where appropriate, of relevant passages	Relevant to claim	CLASSIFICATION OF THE APPLICATION (Int.Cl.6)
X	US-A-4 845 552 (JAGGI) * column 1, paragraph 1 * * column 1, line 61 - line 65 * * column 5, line 54 - line 59 * * column 5, line 65 - column 6, line 7 * * column 7, line 19 - line 21 * * column 7, line 31 - column 8, line 16 * * column 8, line 51 - column 9, line 10 *	1-5, 7-10,12, 14-21, 24,25, 28,37-40	G01N15/14
Y	* figures *	2,13,23, 26,29-36	
Y	APPLIED OPTICS, vol. 26, no. 16, 15 August 1987 NEW YORK US, pages 3315-3324, J.H. TUCKER ET AL 'Automated densitometry of cell populations in a continuous-motion imaging cell scanner' * page 3315, right column, line 15 - line 29 * * page 3317, right column, line 7 - page 3318, left column, line 23; figure 4 *	2,13,23, 29-36	
Y	AIDS, vol. 4, no. 6, 1990 pages 479-497, A. LANDAY ET AL 'Application of flow cytometry to the study of HIV infection' * page 482, left column, line 32 - page 483, left column, line 2 *	26	TECHNICAL FIELDS SEARCHED (Int.Cl.6) G01N
A	* page 484, right column, line 13 - line 19; figures 2,4 *	6,11,22	

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The present search report has been drawn up for all claims

Place of search	Date of completion of the search	Examiner
THE HAGUE	21 August 1995	Thomas, R.M.

CATEGORY OF CITED DOCUMENTS

X : particularly relevant if taken alone
Y : particularly relevant if combined with another document of the same category
A : technological background
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T : theory or principle underlying the invention
E : earlier patent document, but published on, or after the filing date
D : document cited in the application
L : document cited for other reasons
& : member of the same patent family, corresponding document

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DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document with indication, where appropriate, of relevant passages	Relevant to claim	CLASSIFICATION OF THE APPLICATION (Int.Cl.6)
A	US-A-5 107 422 (KAMENTSKY) * abstract * * column 15, line 36 - line 48 * * column 17, line 32 - line 41 * * column 17, line 60 - line 65 * * column 18, line 24 - line 29 * * column 20, line 23 - line 54 * * column 21, line 39 - line 45 * * figures 4,7,8 * ---	1,2,8, 29,34, 37,38	
A	US-A-3 900 265 (MERLEN) * abstract * * column 11, line 21 - line 31 * * column 11, line 52 - line 55 * * figure 1 * -----	2,29,34	
			TECHNICAL FIELDS SEARCHED (Int.Cl.6)

The present search report has been drawn up for all claims

Place of search	Date of completion of the search	Examiner
THE HAGUE	21 August 1995	Thomas, R.M.